

# FIGURE 1A-1E5E3C

1 M A L R R S M G R P G L P P L P P P R L G L L L A A L A S  
 1 CCGCCGATGG CGCTAGGCG GAGCATGGG CGCGCGGGG TCCCGCGCT GCGCTGGCG CGCCACCGC GCGCTGGCT GCTCTGGCTT  
 33 L L L P E S A A A G L K L M G A P V K L T V S Q G Q P V K L N C S  
 101 CTCTGCTGCT CCGGAGTCC GCGCGCGCAG GTCTGAAGCT CATGGGAGCC CCGGTGAAGC TGACAGTGC TCAGGGGCG CCGGTGAAGC TCAACTGCAG  
 66 V E G M E E P D I Q W V K D G A V V Q N L D Q L Y I P V S E Q H W  
 201 TGTGGAGGG ATGGAGGAGC CTGACATCCA GTGGGTGAAG GATGGGGCTG TGGTCCAGAA CTTGGACCAG TTGTACATCC CAGTCAGCGA GCAGCACTGG  
 99 I G F L S L K S V E R S D A G R Y W C Q V E D G G E T E I S O P V W  
 301 ATCGGCTTCC TCAGCCTGAA GTCAGTGGAG CGCTCTGAG CCGGCCGGTA CTGGTGCCAG GTGGAGGATG GGGGTGAAC CGAGATCTCC CAGCCAGTGT  
 133 L T V E G V P F F T V E P K D L A V P P N A P F Q L S C E A V G P  
 401 GGCTCAGGT AGAAGGTGT CCATTTTCA CAGTGGAGCC AAAGATCTG GCAGTGGCC CCAATGCCCC TTTCCAATG TCTTGTGAGG CTGTGGGTCC  
 166 P E P V T I V W W R G T T K I G G P A P S P S V L N V T G V T Q S  
 501 CCTGAACCT GTTACCATTG TCTGGTGGAG AGGAACCTAG AAGATCGGG GACCCGCTCC CTCTCCATCT GTTTAAATG TAACAGGSGT GACCCAGAGC  
 199 T M F S C E A H N L K G L A S S R T A T V H L Q A L P A A P A A P F N I T  
 601 ACCATGTTTT CCTGTGAAGC TCAACACCTA AAAGGCCCTG CCTCTTCTG CACAGCCACT GTTACCTTC AAGCACTGCC TGCAGCCCCC TTCAACATCA  
 233 V T K L S S S N A S V A W M P G A D G R A L L Q S C T V Q V T Q A  
 701 CCGTGACAA GCTTCCAGC AGCAACGCTA GTGTGGCCTG GATGCCAGT GCTGATGCC GAGCTCTGCT ACAGTCTGT ACAGTTCAGG TGACACAGGC  
 266 P G G W E V L A V V V P V P P F T C L L R D L V P A T N Y S L R V  
 801 CCAGGAGGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTA CTGCTGCTG CCGGACCTG GTGCCCTGCA CCAACTACAG CCTCAGGSGT  
 299 R C A N A L G P S P Y A D W V P F Q T K G L A P A S A P Q N L H A I  
 901 CGCTGTGCA ATGCTTGGG GCGCTCTCC TATGCTGACT GGTGCGCTT TCAGACCAAG GGTCTAGCCC CAGCCAGCGC TCCCCAAAC CTCCATGCCA  
 333 R T D S G L I L E W E E V I P E A P L E G P L G P Y K L S W V Q D  
 1001 TCCGCACAGA TTCAGGCTC ATCTTGGAGT GGAAGNAAGT GATCCCGAG GCGCCCTTGG AAGGCCCTT GGGACCTTAC AAAGTGTCT GGTTCAGA  
 366 N G T Q D E L T V E G T R A N L T G W D P Q K D L I V R V C V S N  
 1101 CAATGGAAC CAGGATGAGC TGACAGTGA GGGGACAGG GCCAATTGA CAGGCTGGGA TCCCCAAAG GACCTGATCG TACGTGTGCG CGTCTCCAAT  
 399 A V G C G P W S Q P L V V S S H D R A G Q Q G P P H S R T S W V P V  
 1201 GCAGTTGGCT GTGGACCTCG GAGTCAGCCA CTGGTGTCT CTCTCATGA CCGTGAGGC CAGCAGGSC CTCCTACAG CCGCACATCC TGGGTACCTG  
 433 V L G V L T A L V T A A A L A L I L L R K R R K E T R F G Q A F D  
 1301 TGGTCTTGG TGTGCTAAG GCGCTGTGC CCGCTGCTC ATCTGCTTC GAAAGAGACG GAAAGAGACG CGTTTGGGC AAGCCTTGA

466 S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L  
1401 CAGTGTCTG GCCCGGGAG AGCCAGCGT TCACTTCCGG GCAGCCCGT CCTTCAATCG AGAAGGCC GAGCGCATCG AGCCACATT GGACAGCTTG  
499 G I S D E L K E K L E D V L I P E Q Q F T L G R M L G K G E F G S V  
1501 GGCATCAGCG ATGAATAA GGAATACTG GAGGATGTGC TCATCCCA GACAGCATTC ACCCTGGGCC GGATGTTGG CANAGGAGAG TTTGGTTCAG  
533 R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E F  
1601 TGCGGAGGC CCAGCTGAAG CAAGAGGATG GCTCCTTTGT GAAAGTGCT GTGAGATGC TGAAGCTGA CATCATTTGCC TCAAGCGACA TTGAAGAGTT  
566 L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I  
1701 CCTCAGGAA GCAGCTTGCA TGAAGGAGTT TGACCATCCA CACGTGGCCA AACTTGTGG GGTAAAGCCTC CGGAGCAGG CTAAAGGCCG TCTCCCATC  
599 P M V I L P F M K H G D L H A F L L A S R I G E N P F N L P L Q T L  
1801 CCCATGTCA TCTTGCCCTT CATGAGCAT GGGGACCTGC ATGCCCTTCT GCTCGCCTCC CGGATTGGG AGAACCCCTT TAACCTACCC CTCCAGACCC  
633 I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A E  
1901 TGATCCGTT CATGTTGAC ATTGCTTCCG GCATGGAGTA CCTGAGCTCT CGGAATCTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA  
666 D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W  
2001 GGACATGACA GTGTGTGTGG CTGACTTCCG ACTCTCCCG AGATCTACA GTGGGACTA CTATCGTCAA GGCTGTGCT CCAAACTGCC TGTCAAAGTGG  
699 L A L E S L A D N L Y T V Q S D V W A F G V T M W E I M T R G Q T P  
2101 CTGGCCCTGG AGAGCCTGCC CGACAACCTG TATACTGTGC AGAGTGACGT GTGGCGTTC GGGGTGACCA TGTGGGAGAT CATGACACGT GGGCAGACGC  
733 Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L M  
2201 CATATGCTGG CATCGAAAC GCTGAGATT ACAACTACCT CATTTGGCGG AACCGCCTGA AACAGCCTCC GGAGTGTATG GAGGACGTGT ATGATCTCAT  
766 Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A  
2301 GTACCACTGC TGGAGTGCTG ACCCAAGCA GCGCCCGAGC TTTACTTGTG TCGGAATGGA ACTGGAGAAC ATCTTGGGCC AGCTGTCTGT GCTATCTGCC  
799 S Q D P L Y I N I E R A E E P T A G G S L E L P G R D Q P Y S G A G  
2401 AGCCAGGACC CCTTATACAT CAACATCAG AGAGCTGAG AGCCCACTGC GGGAGGCAGC CTGGAGCTAC CTGGCAGGGA TCAGCCCTAC AGTGGGGCTG  
833 D G S G M G A V G G T P S D C R Y I L T P G G L A E Q P G Q A E H  
2501 GGGATGGCAG TGGCATGGG GCAGTGGGTG GCACTCCCAG TGACTGTGCG TACATACTCA CCCCCGAGG GCTGGCTGAG CAGCCAGGCC AGGCAGAGCA  
866 Q P E S P L N E T Q R L L L L Q Q G L L P H S S C O  
2601 CCAGCCAGAG AGTCCCCTCA ATGAGACACA GAGGCTTTTG CTGCTGCAGC AAGGGCTACT GCCACACAGT AGCTGTTAGC CCACAGCAG AGGGCATCGG  
2701 GGCCATTGG CCGGCTCTGG TGGCCACTGA GCTGGCTGAC TAAGCCCCGT CTGACCCCG AGGTGTGGA GGCTCTGTG GTAGTCTCTC  
2801 CAAGCTGTG TGGGAGGCC GGA CTGACCA ANTCACCAA TCCAGTTCT TCCTGCAACC ACTCTGTGGC CAGCCTGGCA TCAGTTTAGG CCTTGGCTTG

FIGURE 1A-3

2901 ATGGAAGTGG GCCAGTCCCTG GTTGCTCTGAA CCCAGGCAGC TGGCAGGAGT GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTGTGGGG  
 3001 AGGGCAGGTC CAGCTCTGTG GGCCCTACCC TCCTGCTGAG CTGCCCCCTGC TGCTTAAAGT CATGCATTGA GCTGCCCTCCA GCCTGGTGGC CCAGCTATTA  
 3101 CCACACTTGG GGTTTAAATA TCCAGGTGTG CCCCTCCAAG TCACAAAGAG ATGTCCCTTGT AATATTCCCT TTTAGGTGAG GGTGGTAAG GGGTTGGTAT  
 3201 CTCAGGTCTG AATCTTCACC ATCTTTCTGA TTCCGACACC TGCCTACGCC AGGAGAAGTT GAGGGGAGCA TGCTTCCCTG CAGCTGACCG GGTACACAAA  
 3301 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCCCTCTC CAAAGGCAGC GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTTGC CCAGGAGCAA  
 3401 GTGAGGCCGG AGAGGAGTTC AGGAACCCCTT CTCCATACCC ACAATCTGAG CACGCTACCA AATCTCAAAA TATCCTAAGA CTAACAAAGG CAGCTGTGTC  
 3501 TGAGCCCCAAC CCTTCTAAAC GGTGACCTTT AGTGCCCACT TCCCCCTCTAA CTGGACAGCC TCCTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCCTGATG  
 3601 AGGGGAATT C

# FIGURE 1

1 CCTCCGCCAC CCTCCTCTCA GCGCTCGGG GCGGGGCCG GCATGGTGG CGTCGCCGCC GATGGCGCTG AGCGGAGCA TGGGTGGCC GGGCTCCGG

14 P L L L A G L A S L L L P G S A A A G L K L M G A P V K M T V S Q G

101 CCGCTGCTG TGGCGGACT GGCCTCTCTG CTGCTCCCG GGTCTCGGC CGCAGGCTG AGCTCATGG GCGCCCACT GAAGATGACC GTGTCTCAGG

48 Q P V K L N C S V E G M E D P D I H W M K D G T V V Q N A S Q V S

201 GGCAGCCAGT GAAGCTCAAC TGCAGCTGG AGGGATGGA GGACCTGAC ATCCACTGGA TGAAGGATGG CACCGTGGT CAGAATGCA GCCAGGTGTC

81 I S I S E H S W I G L L S L K S V E R S D A G L Y W C Q V K D G E

301 CATCTCCATC AGCAGCACA GCTGGATTGG CTTACTCAGC CTAAGTCAG TGGAGCGGTC TGATGCTGGC CTGACTGGT GCCAGGTGAA GGATGGGAG

114 E T K I S Q S V W L T V E G V P F F T V E P K D L A V P P N A P F Q

401 GAAACCAAGA TCTCTCAGTC AGTATGGCTC ACTGTGMA GGTGTCCATT CTTACACAGT GAACCAAG ATCTGGCGGT GCCACCAAT GCCCTTTTC

148 L S C E A V G P P E P V T I Y W W R G L T K V G G P A P S P S V L

501 AGCTGCTTG TGAGGCTGT GGTCTCTCAG AACCGTAAC CATTACTGG TGGAGAGGAC TCACTAAGGT TGGGGACCT GCTCCCTCTC CCTCTGTTTT

181 N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L Q A

601 AAATGTGACA GGAGTGACC AGGCACAGA GTTTCTTGT GAAGCCCGCA ACATAAAG CCTGGCCACT TCCGACCAG CCATTGTTG CCTTCAAGCA

214 P P A A P F N T T V T T I S S Y N A S V A W V P G A D G L A L L H S

701 CCGCTGCAG CTCCTTTCAA CACCACAGTA ACAACGATCT CCAGCTACAA CGTAGCGTG GCCTGGGTG CAGGTGCTGA CCGCTAGCT CTGCTGCATT

248 C T V Q V A H A P G E W E A L A V V V P V P P F T C L L R N L A P

801 CCTGTACTGT ACAGGTGGCA CACGCCCCAG GAGATGGA GGCCTTGTCT GTTGTGGTTC CTGTGCCACC TTTTACCTGC CTGCTTCGA ACTTGGCCCC

281 A T N Y S L R V R C A N A L G P S P Y G D W V P F Q T K G L A P A

901 TGCCACCAAC TACAGCCTTA GGTGCGGTG TGCCAATGCC TTGGGCCCTT CTCCTACCG CGACTGGGTG CCCTTTCAGA CAAAGGCGCT AGCGCCAGCC

314 R A P Q N F H A I R T D S G L I L E W E E V I P E D P G E G P L G P

1001 AGAGCTCCTC AGAATTTCCA TGCCATTGCT ACCGACTCAG GCCTTATCTT GGAATGGAA GAAGTGATTC CTGAAGACC TGGGAAGGC CCCCTAGGAC

348 Y K L S W V Q E N G T Q D E L M V E G T R A N L T D W D P Q K D L

1101 CTTATAAGCT GTCCTGGGTC CAAGAAATG GAACCCAGGA TGAGTGTATG GTGGAAGGA CCAGGCCAA TCTGACCGAC TGGGATCCCC AGAAGGACCT

381 I L R V C A S N A I G D G P W S Q P L V V S S H D H A G R Q G P P

1201 GATTTTGGGT GTGTGTCCT CCAATGCAAT TGGTGATGG CCCTGGAGTC AGCCACTGCT GGTGTCTTCT CATGACCATG CAGGAGGCA GGGCCCTCCG

414 H S R T S W V P V V L G V L T A L I T A A A L A L I L L R K R R K E

1301 CACAGCCGCA CATCTGGGT GCCTGTGGTC CTGGCGGTG TCACGCCCTT GATCAGACT GCTGCGTGG CCCTCATCCT GCTTCGGAAG AGCGCAAGG

448 T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E R

1401 AGACGCTTT CGGCAAGCC TTGACAGTG TCATGGCCCG AGGGAGCCA GCTGTACACT TCCGGCAGC CCGATCTTTC AATCGAGAAA GGCCTGAACG

## Figure 1B-2

481 I E A T L D S L G I S D E L K E K L E D V L I P E Q Q F T L G R M  
1501 CATTGAGGCC ACATTGGATA GCTGGGCAT CAGCATGAA TTGAAGGAA AGCTGGAGGA TGCTCTCAT CCAGAGCAGC AGTTCACCT CGTCCGATG  
514 L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I  
1601 TTGGGCAAG GAGATTGG ATCAGTGCAG GAGCCAGC TAAAGCAGGA AGATGGCTCC TTGCTGAAG TGGCAGTGA GATCTGAAA GCTGACATCA  
548 A S S D I E E F L R E A A C M K E F D H P H V A K L V G V S L R S  
1701 TTGCCTCAAG CGACATAGAA GTGTTCTCC GGAAGCAGC TTGCATGAG GAGTTTGACC ATCCACAGCT GGCAGAGCTT GTTGGGTGA GCCTCCGAG  
581 R A K G R L P I P M V I L P F M K H G D L H A F L L A S R I G E N  
1801 CAGGCTAAA GGTGCTCTCC CCATTCCCAT GGTATCCCTG CCCTTCATGA AACATGGAGA CTTCACGCC TTCTGTCTCG CCTCCGAAT CGGGAGAAC  
614 P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A  
1901 CCTTTAAAC TGCCCTGCA GACCTGGTC CGTTTCATGG TGGACATTCG CTGTGCGATG GAGTACCTGA GCTCCCGGA CTTCATCCAC CGAGACCTAG  
648 A R N C M L A E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C  
2001 CAGTCGGAA TTGCATGCTG GCGAGGACA TGACAGTGTG TGTGGCTGAT TTGCACTCT CTCGGAAT CTATAGCGG GACTATTATC GTCAGGGCTG  
681 A S K L P V K W L A L E S L A D N L Y T V H S D V W A F G V T M W  
2101 TGCTCCCAA TTGCCGTCA AGTGGCTGGC CTGGAGAGC TTGGCTGACA ACTGTATAC TGTACACAGT GATGTGGG CCTTCGGGT GACCATGTG  
714 E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C  
2201 GAGATCATGA CTCGTGGCA GAGCCATAT GCTGGCATG AAATGCTGA GATTACAA TACCTCATG GCGGAACCG CCTGAAGCAG CCTCCGGAGT  
748 M E E V Y D L M Y Q C W S A D P K Q R P S F T C L R M E L E N I L  
2301 GCATGGAGGA AGTGATGAT CTCATGTACC AGTGTGGAG CGCCGACCCC AAGCAGGCC CAAGTTCAC GTGTCTCGA ATGGAACCTG AGAACATTCT  
781 G H L S V L S T S Q D P L Y I N I E R A E Q P T E S G S P E L H C  
2401 GGGCACCTG TCTGTGCTGT CCACCAGCA GGACCCCTG TACATCAACA TTGAGAGAGC TGAGCAGCCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT  
814 G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S  
2501 GGAGAGCAT CCAGCAGCA GGCAGGGAC GGCAGTGGC TGGGGCAGT AGGTGGCATC CCCAGTACT CTCGGTACAT CTTAGCCCC GGAGGGCTAT  
848 E S P G Q L E Q Q P E S P L N E N Q R L L L L Q Q G L L P H S S C  
2601 CCAGTCACC AGGCAGCTG GAGCAGCAGC CAGAAAGCCC CCTCAATGAG AACAGAGGC TGTGTGCTG GCAGCAAGG CTACTGCCTC ACAGTAGCTG  
881 O  
2701 TTAACCTCA GGCAGAGGA AGTTGGGGC CCTGGCTCTG CTGACCGCTG CTAGGCCAG TCTGATCACA GCCAGGCAG CAAGGTATGG  
2801 AGGCTCCTGT GTAGCCCTC CCAAGCTGTG TGGGCTCTG ACGGACCAA TTGCCCAATC CCAGTTCTTC CTGAGCCGC TCTGGCCAG CTGGCATCAG  
2901 TTCAGGCCTT GGCTTAGAG AGGTGAGCA GAGTGGTTG CCTGAATGCA GGCAGCTGGC AGGAGGGAG GGTGGCTATG TTTCCATGG TACCATGGGT  
3001 GTGGATGCA GTAAGGGAG GTAGCAACAG CCTGTGGCC CCTACCTCC TGGCTGAGT GTCCTACTT TAGTGCATG TTGAGCCGC CTGACGCTG  
3101 GAACTACGA CTGCCCCACCA CACTTGGGC GAATGGCCAG GTTGGCCCT CTTAAGTCAC AAAGAGATGT CCATGTATTG TTCCCTTTA GGTGATGATT

FIGURE 1B-3

3201 AGGAAGGGAT TGGCACACTT GGTCCCTAA GCCCTATGGC AGGAATGGT GGGATATTCT CAGGTCTGAA TCCTCATCAT CTTCTGATT CCCCACCCCTG  
 3301 CAAAGGCCCTG GAACTGGCTG TGGGGCTCTG ACGCATGCTG AAGGACAAAA GGTACAGAG ATCCGACTTC AAGAGGCAGG GTCTGAGTCT GGCAGGTGGA  
 3401 GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTTCAG ACCCCTCCAA GCTTCTACAG TCTGTCTGAG CATGCTACCA AGCCCCCAGA TACCCCAAAA  
 3501 CTAACAGAGG CAGTTTGTG TGAGCCCAGC CCTCCCACAT GATGACCCCTT AGGTCTACCC TCCTCTCTAA ATGGACATCC TCGTTTGTCC CAAGTCTCCA  
 3601 GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAGGG CTGGGGTGGA ACCAGGGCTG GGGTCGAGGC AGGCTCTTGG GCAGGCTCTT  
 3701 GCTGTTAGGA ACATTTCTAA GCTATTAACT TGCTGTTTCA AAACAAATAA AATTGAAACA TAAAGAAATCA AAAAAAAAAA AAAAA

# FIGURE 2 -1

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1 GAATTCTCGA GTCGACGTTG GACTTGAAGG AATGCCAAGA GATGCTGCCC
51 CCACCCCCTT AGGCCCGAGG GATCAGGAGC TATGGGACCA GAGGCCCTGT
1 MetGlyPro GluAlaLeuSer
*****

101 CATCTTTACT GCTGCTGCTC TTGGTGGCAA GTGGAGATGC TGACATGAAG
8 SerLeuLe uLeuLeuLeu LeuValAlaS erGlyAspAl aAspMetLys
*****

151 GGACATTTTG ATCCTGCCAA GTGCCGCTAT GCCCTGGGCA TGCAGGACCG
24 GlyHisPheA spProAlaLy sCysArgTyr AlaLeuGlyM etGlnAspArg

201 GACCATCCCA GACAGTGACA TCTCTGCTTC CAGCTCCTGG TCAGATTCCA
41 ThrIlePro AspSerAspI leSerAlaSe rSerSerTrp SerAspSerThr

251 CTGCCGCCCCG CCACAGCAGG TTGGAGAGCA GTGACGGGGA TGGGGCCTGG
58 AlaAlaAr gHisSerArg LeuGluSers erAspGlyAs pGlyAlaTrp

301 TGCCCCGCAG GGTCGGTGTT TCCCAAGGAG GAGGAGTACT TGCAGGTGGA
74 CysProAlaG lySerValPh eProLysGlu GluGluTyrL euGlnValAsp

351 TCTACAACGA CTGCACCTGG TGGCTCTGGT GGGCACCCAG GGACGGCATG
91 LeuGlnArg LeuHisLeuV alAlaLeuVa lGlyThrGln GlyArgHisAla

401 CCGGGGGCCT GGGCAAGGAG TTCTCCCGGA GCTACCGGCT GCGTTACTCC
108 GlyGlyLe uGlyLysGlu PheSerArgS erTyrArgLe uArgTyrSer

451 CGGGATGGTC GCCGCTGGAT GGGCTGGAAG GACCGCTGGG GTCAGGAGGT
124 ArgAspGlyA rgArgTrpMe tGlyTrpLys AspArgTrpG lyGlnGluVal

501 GATCTCAGGC AATGAGGACC CTGAGGGAGT GGTGCTGAAG GACCTTGGGC
141 IleSerGly AsnGluAspP roGluGlyVa lValLeuLys AspLeuGlyPro

551 CCCCCATGGT TGCCCGACTG GTTCGCTTCT ACCCCCGGGC TGACCGGGTC
158 ProMetVa lAlaArgLeu ValArgPheT yrProArgAl aAspArgVal

601 ATGAGCGTCT GTCTGCGGGT AGAGCTCTAT GGCTGCCTCT GGAGGGATGG
174 MetSerValC ysLeuArgVa lGluLeuTyr GlyCysLeuT rpArgAspGly

651 ACTCCTGTCT TACACCGCCC CTGTGGGGCA GACAATGTAT TTATCTGAGG
191 LeuLeuSer TyrThrAlaP roValGlyGl nThrMetTyr LeuSerGluAla

701 CCGTGTACCT CAACGACTCC ACCTATGACG GACATACCGT GGGCGGACTG
208 ValTyrLe uAsnAspSer ThrTyrAspG lyHisThrVa lGlyGlyLeu

751 CAGTATGGGG GTCTGGGGCA GCTGGCAGAT GGTGTGGTGG GGCTGGATGA
224 GlnTyrGlyG lyLeuGlyGl nLeuAlaAsp GlyValValG lyLeuAspAsp

801 CTTTAGGAAG AGTCAGGAGC TCGGGTCTG GCCAGGCTAT GACTATGTGG
241 PheArgLys SerGlnGluL euArgValTr pProGlyTyr AspTyrValGly

851 GATGGAGCAA CCACAGCTTC TCCAGTGGCT ATGTGGAGAT GGAGTTTGAG
258 TrpSerAs nHisSerPhe SerSerGlyT yrValGluMe tGluPheGlu

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Figure 2-2

901 TTTGACCGGC TGAGGGCCTT CCAGGCTATG CAGGTCCACT GTAACAACAT  
 274 PheAspArgL euArgAlaPh eGlnAlaMet GlnValHisC ysAsnAsnMet  
 951 GCACACGCTG GGAGCCCGTC TGCCTGGCGG GGTGGAATGT CGCTTCCGGC  
 291 HisThrLeu GlyAlaArgL euProGlyGl yValGluCys ArgPheArgArg  
 1001 GTGGCCCTGC CATGGCCTGG GAGGGGGAGC CCATGCGCCA CAACCTAGGG  
 308 GlyProAl aMetAlaTrp GluGlyGluP roMetArgHi sAsnLeuGly  
 1051 GGCAACCTGG GGGACCCAG AGCCCGGGCT GTCTCAGTGC CCCTTGGCGG  
 324 GlyAsnLeuG lyAspProAr gAlaArgAla ValSerValP roLeuGlyGly  
 1101 CCGTGTGGCT CGCTTTCTGC AGTGCCGCTT CCTCTTTGCG GGGCCCTGGT  
 341 ArgValAla ArgPheLeuG lnCysArgPh eLeuPheAla GlyProTrpLeu  
 1151 TACTCTTCAG CGAAATCTCC TTCATCTCTG ATGTGGTGAA CAATTCCTCT  
 358 LeuPheSe rGluIleSer PheIleSerA spValValAs nAsnSerSer  
 1201 CCGGCACTGG GAGGCACCTT CCCGCCAGCC CCCTGGTGGC CGCCTGGCCC  
 374 ProAlaLeuG lyGlyThrPh eProProAla ProTrpTrpP roProGlyPro  
 1251 ACCTCCCACC AACTTCAGCA GCTTGGAGCT GGAGCCCAGA GGCCAGCAGC  
 391 ProProThr AsnPheSerS erLeuGluLe uGluProArg GlyGlnGlnPro  
 1301 CCGTGGCCAA GCCCGAGGGG AGCCCGACCG CCATCCTCAT CGGCTGCCTG  
 408 ValAlaLy sProGluGly SerProThrA laIleLeuIl eGlyCysLeu  
 1351 GTGGCCATCA TCCTGCTCCT GCTGCTCATC ATTGCCCTCA TGCTCTGGCG  
 424 ValAlaIleI leLeuLeuLe uLeuLeuIle IleAlaLeuM etLeuTrpArg  
 1401 GCTGCACTGG CGCAGGCTCC TCAGCAAGGC TGAACGGAGG GTGTTGGAAG  
 441 LeuHisTrp ArgArgLeuL euSerLysAl aGluArgArg ValLeuGluGlu  
 1451 AGGAGCTGAC GGTTACCTC TCTGTCCCTG GGGACACTAT CCTCATCAAC  
 458 GluLeuTh rValHisLeu SerValProG lyAspThrIl eLeuIleAsn  
 1501 AACCGCCAG GTCCTAGAGA GCCACCCCG TACCAGGAGC CCCGGCCTCG  
 474 AsnArgProG lyProArgGl uProProPro TyrGlnGluP roArgProArg  
 1551 TGGGAATCCG CCCCCTCCG CTCCCTGTGT CCCCATGGC TCTGCGTTGC  
 491 GlyAsnPro ProHisSerA laProCysVa lProAsnGly SerAlaLeuLeu  
 1601 TGCTCTCCAA TCCAGCCTAC CGCCTCCTT TGGCCACTTA CGCCCGTCCC  
 508 LeuSerAs nProAlaTyr ArgLeuLeuL euAlaThrTy rAlaArgPro  
 1651 CCTCGAGGCC CGGGCCCCC CACACCCGCC TGGGCCAAAC CCACCAACAC  
 524 ProArgGlyP roGlyProPr oThrProAla TrpAlaLysP roThrAsnThr  
 1701 CCAGGCCTAC AGTGGGGACT ATATGGAGCC TGAGAAGCCA GGCGCCCCG  
 541 GlnAlaTyr SerGlyAspT yrMetGluPr oGluLysPro GlyAlaProLeu  
 1751 TTCTGCCCCC ACCTCCCCAG AACAGCGTCC CCCATTATGC CGAGGCTGAC  
 558 LeuProPr oProProGln AsnSerValP roHisTyrAl aGluAlaAsp

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**096260 - DLT-01**

1801	ATTGTTACCG	TGCAGGGCGT	CACCGGGGGC	AACACCTATG	CTGTGCCTGC
574	IleValThrL	euGlnGlyVa	lThrGlyGly	AsnThrTyrA	laValProAla
1851	ACTGCCCCCA	GGGGCAGTCG	GGGATGGGCC	CCCCAGAGTG	GATTTCCCTC
591	LeuProPro	GlyAlaValG	lyAspGlyPr	oProArgVal	AspPheProArg
1901	GATCTCGACT	CCGCTTCAAG	GAGAAGCTTG	GCGAGGGCCA	GTTTGGGGAG
608	SerArgLe	uArgPheLys	GluLysLeuG	lyGluGlyGl	nPheGlyGlu
	<< <		.	.....	.....
1951	GTGCACCTGT	GTGAGGTCGA	CAGCCCTCAA	GATCTGGTCA	GTCTTGATTT
624	ValHisLeuC	ysGluValAs	pSerProGln	AspLeuValS	erLeuAspPhe
2001	CCCCCTTAAT	GTGCGTAAGG	GACACCCTTT	GCTGGTAGCT	GTCAAGATCT
641	ProLeuAsn	ValArgLysG	lyHisProLe	uLeuValAla	ValLysIleLeu
2051	TACGGCCAGA	TGCCACCAAG	AATGCCAGGA	ATGATTTCTT	GAAAGAGGTG
658	ArgProAs	pAlaThrLys	AsnAlaArgA	snAspPheLe	uLysGluVal
2101	AAGATCATGT	CGAGGCTCAA	GGACCCAAAC	ATCATTCGGC	TGCTGGGCGT
674	LysIleMetS	erArgLeuLy	sAspProAsn	IleIleArgL	euLeuGlyVal
2151	GTGTGTGCAG	GACGACCCCC	TCTGCATGAT	TACTGACTAC	ATGGAGAACG
691	CysValGln	AspAspProL	euCysMetIl	eThrAspTyr	MetGluAsnGly
2201	GCGACCTCAA	CCAGTTCCTC	AGTGCCCACC	AGCTGGAGGA	CAAGGCAGCC
708	AspLeuAs	nGlnPheLeu	SerAlaHisG	lnLeuGluAs	pLysAlaAla
2251	GAGGGGGCCC	CTGGGGACGG	GCAGGCTGCG	CAGGGGGCCA	CCATCAGCTA
724	GluGlyAlaP	roGlyAspGl	yGlnAlaAla	GlnGlyProT	hrIleSerTyr
2301	CCCAATGCTG	CTGCATGTGG	CAGCCCAGAT	CGCCTCCGGC	ATGCGCTATC
741	ProMetLeu	LeuHisValA	laAlaGlnIl	eAlaSerGly	MetArgTyrLeu
2351	TGGCCACACT	CAACTTTGTA	CATCGGGACC	TGGCCACGCG	GAAGTGCCTA
758	AlaThrLe	uAsnPheVal	HisArgAspL	euAlaThrAr	gAsnCysLeu
2401	GTTGGGGAAA	ATTTACCAT	CAAAATCGCA	GACTTTGGCA	TGAGCCGGAA
774	ValGlyGluA	snPheThrIl	eLysIleAla	AspPheGlyM	etSerArgAsn
2451	CCTCTATGCT	GGGGACTATT	ACCGTGTGCA	GGGCCGGGCA	GTGCTGCCCA
791	LeuTyrAla	GlyAspTyrT	yrArgValGl	nGlyArgAla	ValLeuProIle
2501	TCCGCTGGAT	GGCCTGGGAG	TGCATCCTCA	TGGGGAAGTT	CACGACTGCG
808	ArgTrpMe	tAlaTrpGlu	CysIleLeuM	etGlyLysPh	eThrThrAla
2551	AGTGACGTGT	GGGCCTTTGG	TGTGACCCTG	TGGGAGGTGC	TGATGCTCTG
824	SerAspValT	rpAlaPheGl	yValThrLeu	TrpGluValL	euMetLeuCys
2601	TAGGGCCCAG	CCCTTTGGGC	AGCTCACCGA	CGAGCAGGTC	ATCGAGAACG
841	ArgAlaGln	ProPheGlyG	lnLeuThrAs	pGluGlnVal	IleGluAsnAla

# FIGURE 2-4

2651 CGGGGGAGTT CTTCCGGGAC CAGGGCCGGC AGGTGTACCT GTCCCGGCCG  
 858 GlyGluPh ePheArgAsp GlnGlyArgG lnValTyrLe uSerArgPro  
 2701 CCTGCCTGCC CGCAGGGCCT ATATGAGCTG ATGCTTCGGT GCTGGAGCCG  
 874 ProAlaCysP roGlnGlyLe uTyrGluLeu MetLeuArgC ysTrpSerArg  
 2751 GGAGTCTGAG CAGCGACCAC CCTTTTCCCA GCTGCATCGG TTCCTGGCAG  
 891 GluSerGlu GlnArgProP roPheSerGl nLeuHisArg PheLeuAlaGlu  
 >>>

2801 AGGATGCACT CAACACGGTG TGAATCACAC ATCCAGCTGC CCCTCCCTCA  
 908 AspAlaLe uAsnThrVal

2851 GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG GACACAATGG

2901 CACCTCTGCC CTTCCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT

2951 GAGACTGCAG AAGCCCCTGT CGCCCACCCA GCTGGTCCTG TGGATGGGAT

3001 CCTCTCCACC CTCCTCTAGC CATCCCTTGG GGAAGGGTGG GGAGAAATAT

3051 AGGATAGACA CTGGACATGG CCCATTGGAG CACCTGGGCC CCACTGGACA

3101 ACACTGATTC CTGGAGAGGT GGCTGCGCCC CCAGCTTCTC TCTCCCTGTC

3151 ACACACTGGA CCCCACTGGC TGAGAATCTG GGGGTGAGGA GGACAAGAAG

3201 GAGAGGAAAA TGTTTCCTTG TGCCTGCTCC TGTACTTGTC CTCAGCTTGG

3251 GCTTCTTCCT CCTCCATCAC CTGAAACACT GGACCTGGGG GTAGCCCCGC

3301 CCCAGCCCTC AGTCACCCCC ACTTCCCACC TGCAGTCTTG TAGCTAGAAC

3351 TTCTCTAAGC CTATACGTTT CTGTGGAGTA AATATTGGGA TTGGGGGGAA

3401 AGAGGGAGCA ACGGCCATA GCCTTGGGGT TGGACATCTC TAGTGTAGCT

3451 GCCACATTGA TTTTCTATA ATCACTTGGG GTTGTACAT TTTGGGGGG

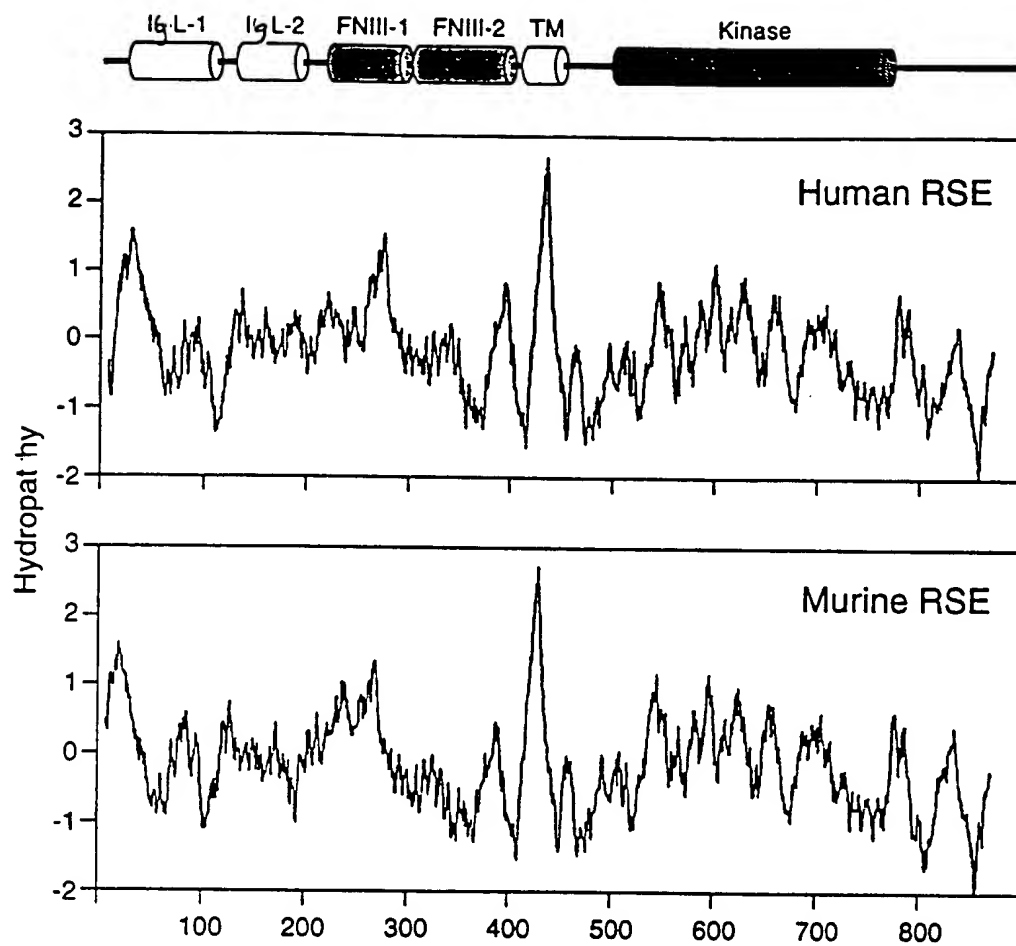
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3551 AATCCCCTGC ACTAGGCAGG TAATAATAAA GGTGAGTTT TCCACAAAAA

3601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

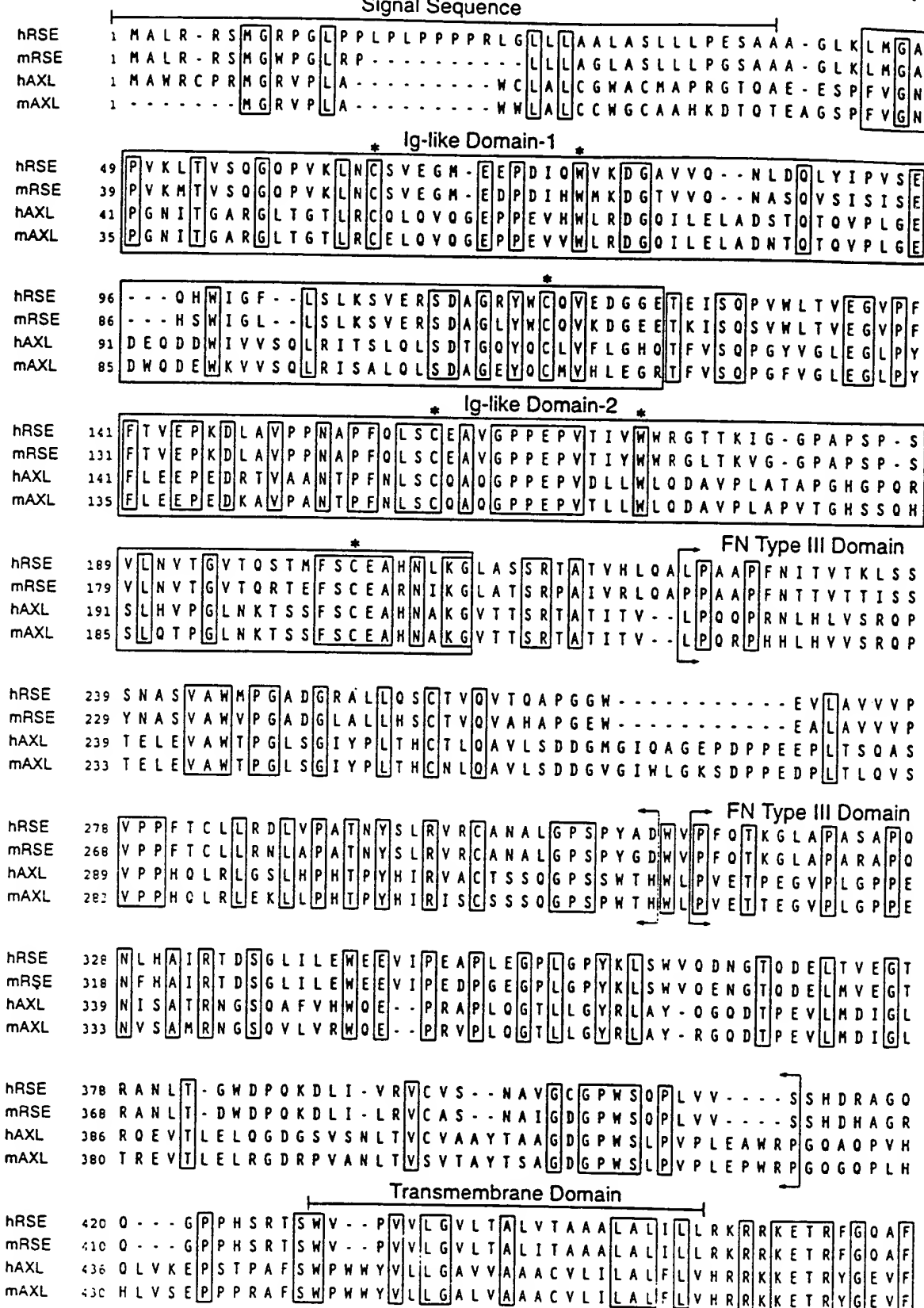
09236939.01259

FIGURE 3



665270" 6E69E260

FIGURE 4-1  
Signal Sequence



**00000000000000000000**

465 DSVMAARGEPAVHFRAARSFNRERPERIEATLDSLGISDELKEKLE<sup>EDV</sup>LIP  
mRSE 455 DSVMAARGEPAVHFRAARSFNRERPERIEATLDSLGISDELKEKLE<sup>EDV</sup>LIP  
hAXL 486 EPTVERGE<sup>LV</sup>VRYRVRKSYSR- - -RTTEATLNSLGISEELKEKLRD<sup>VM</sup>VD  
mAXL 480 EPTVERGE<sup>LV</sup>VRYRVRKSYSR- - -RTTEATLNSLGISEELKEKLRD<sup>VM</sup>VD

I Tyrosine Kinase Domain II

hRSE 515 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E  
mRSE 505 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E  
hAXL 533 R H K V A L G K T L G E G E F G A V M E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D  
mAXL 527 R H K V A L G K T L G E G E F G A V M E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D

III IV V

hRSE 565 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F  
mRSE 555 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F  
hAXL 582 F L S E A V C M K E F D H P N V M R L I G V C F O G S E R E S F P A P V V I L P F M K H G D L H S F  
mAXL 576 F L S E A V C M K E F D H P N V M R L I G V C F O G S D R E G F P E P V V I L P F M K H G D L H S F

VIa VIb

hRSE 615 L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A  
mRSE 605 L L A S R I G E N P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A  
hAXL 632 L L Y S R L G D Q P V Y L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N  
mAXL 626 L L Y S R L G D Q P V F L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N

VII VIII

hRSE 665 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L L P V K W L A L E S L A D N L Y T V Q S D  
mRSE 655 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L L P V K W L A L E S L A D N L Y T V H S D  
hAXL 682 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D  
mAXL 676 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D

IX X

hRSE 715 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E D V Y D L  
mRSE 705 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E E V Y D L  
hAXL 732 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K O P A D C L D G L Y A L  
mAXL 726 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K O P V D F L D G L Y S L

XII

hRSE 765 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A S O D P L Y I N I E R A E E P T  
mRSE 755 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G H L S V L S T S O D P L Y I N I E R A E O P T  
hAXL 782 M S R C W E L N P Q D R P S F T E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G G Y P  
mAXL 776 M S R C W E L N P R D R P S F A E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G S H L

hRSE 815 A G G S L E L P G R D Q P Y S G A G D G S G M G A V G G T P S D C R Y I L T P G G L A E O P G O A E  
mRSE 805 E S G S P E L H C G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S E S P G O L E  
hAXL 832 E P P G A A G G A D P P T O P D P K D S C S C L T A A E V H P A G R Y V L C P S T - T P S P A Q P A  
mAXL 826 E P R G A A G G A D P P T O P D P K D S C S C L T A A D V H S A G R Y V L C P S T - A P G P T L S A

hRSE 865 H O P E S P L N E T Q R L L L L L O O G L L P H S S C  
mRSE 855 Q O P E S P L N E N Q R L L L L L O O G L L P H S S C  
hAXL 881 - D R G S P A A P G Q - - - - - E D G A - - - - -  
mAXL 875 - D R G C P A P P G Q - - - - - E D G A - - - - -

FIGURE 5

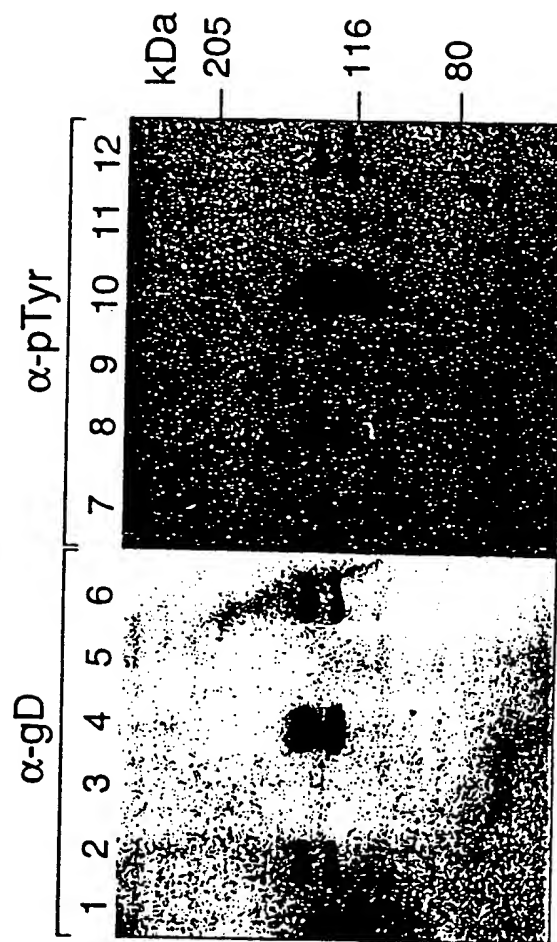
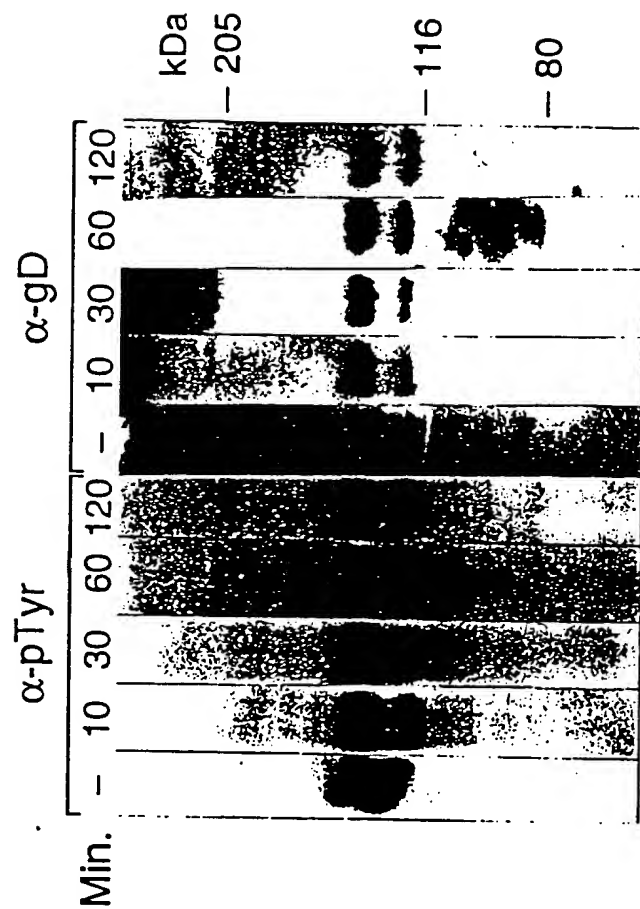


FIGURE 6



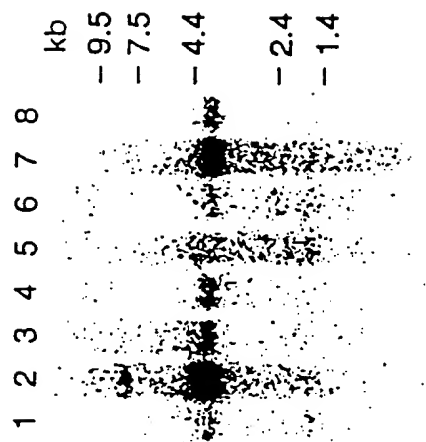


FIGURE 7A



FIGURE 7B



**060901070809**

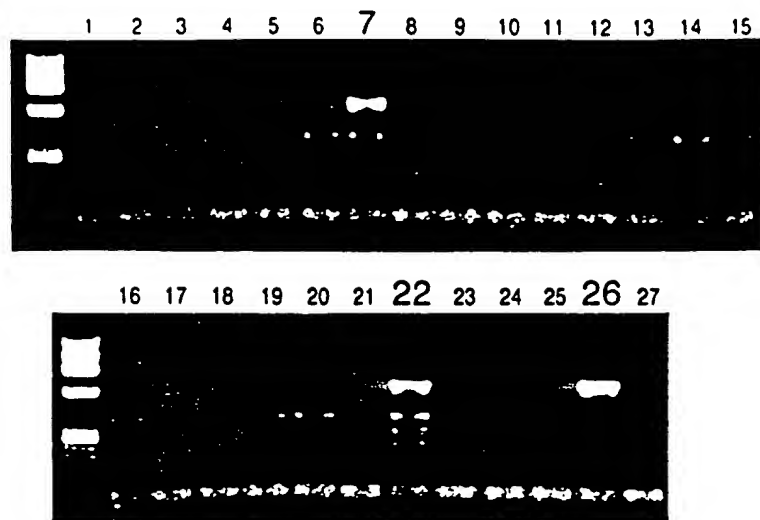


FIGURE 8B

CHROMOSOME CONTENT OF SOMATIC CELL HYBRID PANEL

LANE #	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
CELL LINE	212	324	423	507	683	734	780	784	803	811	852	860	862	867	904	909	937	940	967	968	983	1006	1049	1079	1099
1														*			*								*
2											*														
3			*	*								*												*	
4									*													*			
5	*			*	*	*	*	*	*			*	*	*	*	*	*	*	*	*	*	*	*	*	*
6								*				*			*	*									
7								*														*			
8									*	*						*			*			*			
9					*							*							*						
10											*										*				
11								*															*		
12			*	*				*							*										
13						*	*							*					*						*
14			*	*		*	*							*	*	*									
15					*																*				
16															*				*					*	
17									*								*								
18		*			*					*				*											
19				*		*	*				*		*					*				*			
20				*			*											*							
21				*			*				*			*		*									
22			*					*																*	
23								*							*				*						*
24	*		*		*	*									*					*					

FIGURE 9.

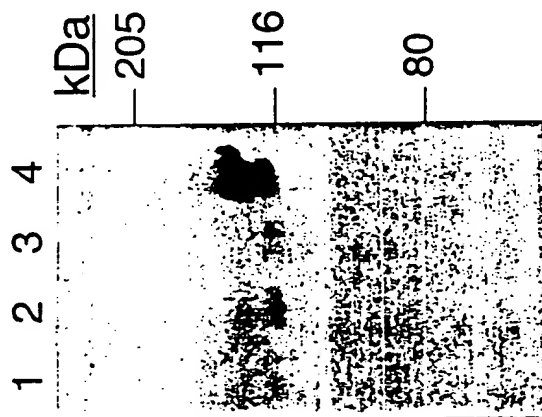


FIGURE 10A.

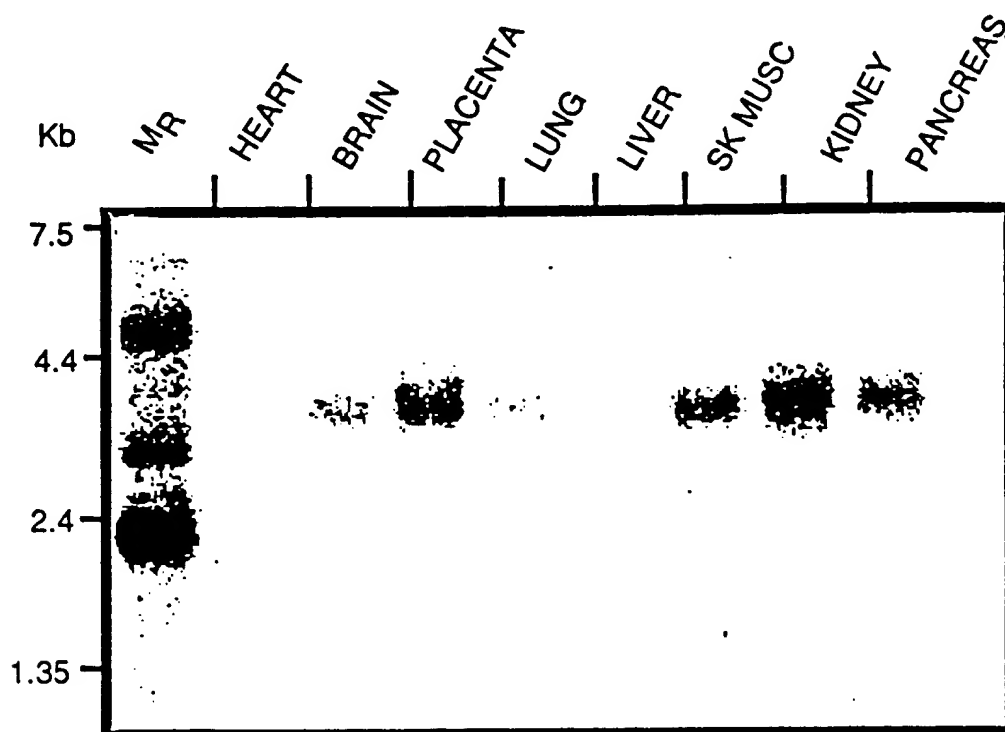
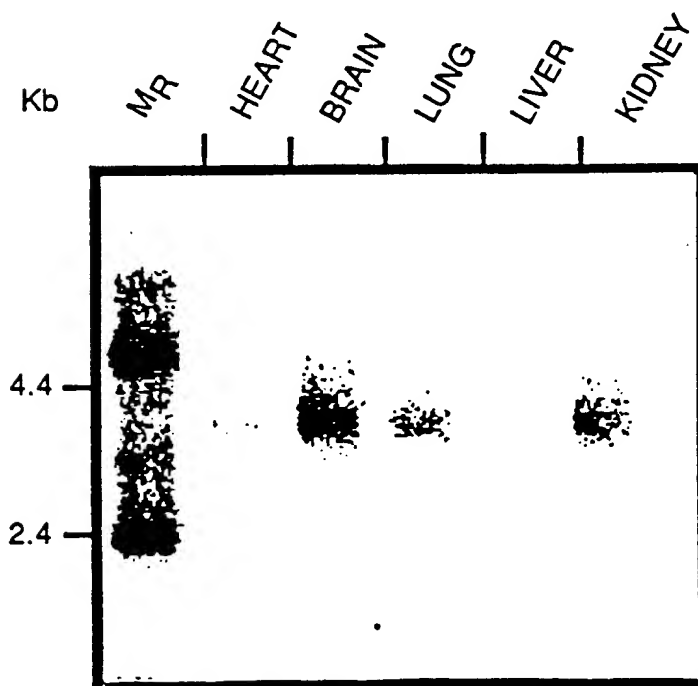


FIGURE 10 B.



665210" 6669E260

665210" 66692260

FIGURE 11A

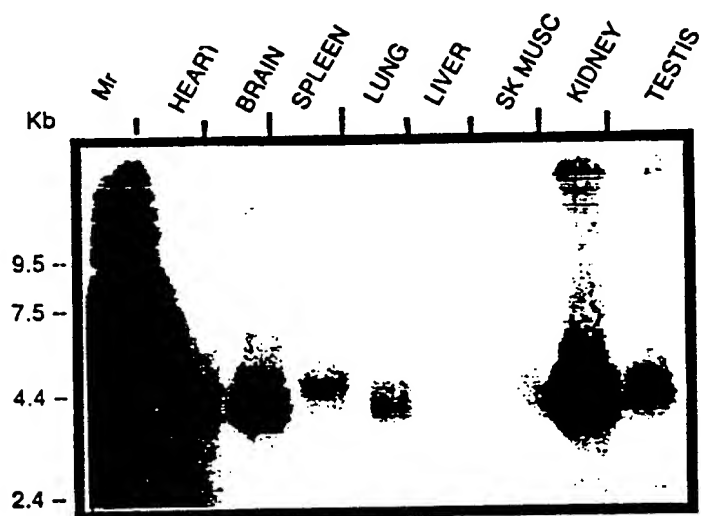


FIGURE 11B

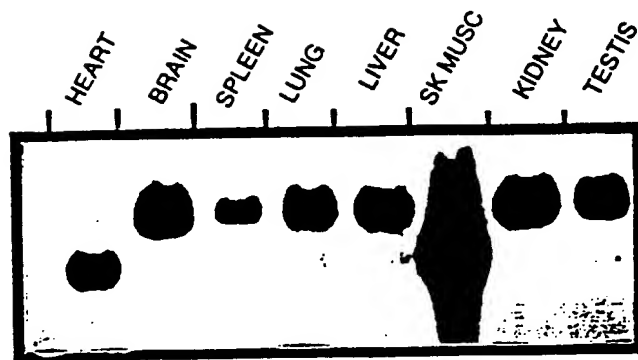


FIGURE 12A  
HUMAN -ve STRAND



FIGURE 12B  
MOUSE -ve STRAND

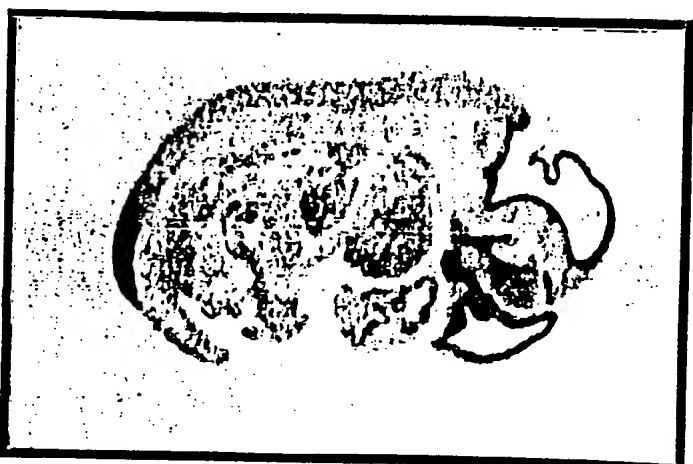
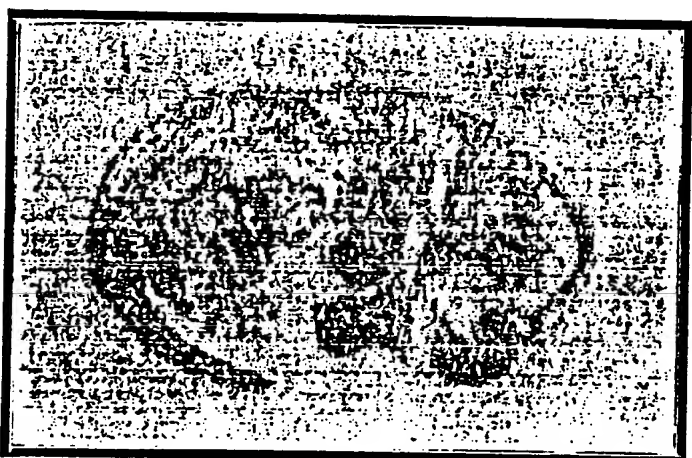


FIGURE 12C  
MOUSE +ve STRAND



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